

SEQUENCE LISTING

<110> Basi, Guriq
Saldanha, Jose
Yednock, Ted

<120> HUMANIZED ANTIBODIES THAT RECOGNIZE
BETA-AMYLOID PEPTIDE

<130> ELN-002CPCN3

<150> US 10/010,942

<151> 2001-12-06

<150> US 60/251,892

<151> 2000-12-06

<160> 63

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 396

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(396)

<221> sig_peptide

<222> (1)...(60)

<400> 1

atg atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cgg	48
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg	
-20 -15 -10 -5	
gaa acc aac ggt tat gtt gtg atg acc cag act cca ctc act ttg tcg	96
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser	
1 5 10	
gtt acc att gga caa cca gcc tcc atc tct tgc aag tca agt cag agc	144
Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser	
15 20 25	
ctc tta gat agt gat gga aag aca tat ttg aat tgg ttg tta cag agg	192
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg	
30 35 40	
cca ggc cag tct cca aag cgc cta atc tat ctg gtg tct aaa ctg gac	240
Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp	
45 50 55 60	
tct gga gtc cct gac agg ttc act ggc agt gga tca ggg aca gat ttt	288
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe	
65 70 75	
aca ctg aaa atc agc aga ata gag gct gag gat ttg gga ctt tat tat	336
Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr	
80 85 90	

tgc tgg caa ggt aca cat ttt cct cgg acg ttc ggt gga ggc acc aag 384
 Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys
 95 100 105

ctg gaa atc aaa 396
 Leu Glu Ile Lys
 110

<210> 2
 <211> 132
 <212> PRT
 <213> Mus musculus

<220>
 <221> SIGNAL
 <222> (1)...(20)

<400> 2
 Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
 -20 -15 -10 -5
 Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser
 1 5 10
 Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
 15 20 25
 Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg
 30 35 40
 Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
 45 50 55 60
 Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
 65 70 75
 Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr
 80 85 90
 Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys
 95 100 105
 Leu Glu Ile Lys
 110

<210> 3
 <211> 414
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(414)

<221> sig_peptide
 <222> (1)...(57)

<400> 3
 atg aac ttc ggg ctc agc ttg att ttc ctt gtc ctt gtt tta aaa ggt 48
 Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
 -15 -10 -5
 gtc cag tgt gaa gtg aag ctg gtg gag tct ggg gga ggc tta gtg aag 96
 Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys
 1 5 10

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cct gga gcg tct ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc 144
Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    15                20                25

agt aac tat ggc atg tct tgg gtt cgc cag aat tca gac aag agg ctg 192
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu
    30                35                40                45

gag tgg gtt gca tcc att agg agt ggt ggt ggt aga acc tac tat tca 240
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
                50                55                60

gac aat gta aag ggc cga ttc acc atc tcc aga gag aat gcc aag aac 288
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
                65                70                75

acc ctg tac ctg caa atg agt agt ctg aag tct gag gac acg gcc ttg 336
Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
    80                85                90

tat tat tgt gtc aga tat gat cac tat agt ggt agc tcc gac tac tgg 384
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
    95                100                105

ggc cag ggc acc act gtc aca gtc tcc tca 414
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110                115

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<210> 4
<211> 138
<212> PRT
<213> Mus musculus

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<220>
<221> SIGNAL
<222> (1)...(19)

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<400> 4
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
                -15                -10                -5
Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys
    1                5                10
Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    15                20                25
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu
    30                35                40                45
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
                50                55                60
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
    65                70                75
Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
    80                85                90
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
    95                100                105
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110                115

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<210> 5
 <211> 132
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> SIGNAL
 <222> (1)...(20)

<223> humanized 3D6 light chain variable region

<400> 5
 Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
 -20 -15 -10 -5
 Glu Thr Asn Gly Tyr Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
 1 5 10
 Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
 15 20 25
 Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys
 30 35 40
 Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
 45 50 55 60
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 65 70 75
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 80 85 90
 Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys
 95 100 105
 Val Glu Ile Lys
 110

<210> 6
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1)...(13)

<400> 6
 Met Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val
 -10 -5 1
 Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
 5 10 15
 Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
 20 25 30 35
 Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
 40 45 50
 Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
 55 60 65
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
 70 75 80
 Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
 85 90 95
 Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 7
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 7
 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Gln Ser Leu Leu His Ser
 20 25 30
 Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95
 Leu Gln Thr Pro
 100

<210> 8
 <211> 138
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized 3D6 heavy chain variable region

<221> SIGNAL
 <222> (1)...(19)

<400> 8
 Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
 -15 -10 -5
 Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 1 5 10
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 15 20 25
 Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 30 35 40 45
 Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Arg Thr Tyr Tyr Ser
 50 55 60
 Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 65 70 75
 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu
 80 85 90
 Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
 95 100 105
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 110 115

<210> 9
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 9
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Val Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Asn Tyr Asp Phe Trp Ser Gly Thr Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 10
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 10
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys

<210> 11
 <211> 132
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> SIGNAL
 <222> (1)...(20)

<223> humanized 3D6 light chain variable region

<400> 11
 Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
 -20 -15 -10 -5

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Glu Thr Asn Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
      1      5      10
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
      15      20      25
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys
      30      35      40
Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
      45      50      55      60
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
      65      70      75
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
      80      85      90
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys
      95      100      105
Val Glu Ile Lys
      110

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<210> 12
<211> 138
<212> PRT
<213> Artificial Sequence

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<220>
<223> Humanized 3D6 light chain variable region

<221> SIGNAL
<222> (1)...(19)

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<400> 12
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
      -15      -10      -5
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
      1      5      10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
      15      20      25
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
      30      35      40      45
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
      50      55      60
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
      65      70      75
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
      80      85      90
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
      95      100      105
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
      110      115

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<210> 13
<211> 393
<212> DNA
<213> Mus musculus

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<220>
<221> CDS
<222> (1)...(393)

<221> sig_peptide
<222> (1)...(57)

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<400> 13

atg	aag	ttg	cct	gtt	agg	ctg	ttg	gta	ctg	atg	ttc	tg	att	cct	gct	48
Met	Lys	Leu	Pro	Val	Arg	Leu	Leu	Val	Leu	Met	Phe	Trp	Ile	Pro	Ala	
				-15					-10					-5		

tcc	agc	agt	gat	gtt	ttg	atg	acc	caa	act	cca	ctc	tcc	ctg	cct	gtc	96
Ser	Ser	Ser	Asp	Val	Leu	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	
		1				5					10					

agt	ctt	gga	gat	caa	gcc	tcc	atc	tct	tgc	aga	tct	agt	cag	aac	att	144
Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Asn	Ile	
	15					20				25						

ata	cat	agt	aat	gga	aac	acc	tat	tta	gaa	tg	tac	ctg	cag	aaa	cca	192
Ile	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	Glu	Trp	Tyr	Leu	Gln	Lys	Pro	
	30				35				40					45		

ggc	cag	tct	cca	aag	ctc	ctg	atc	tac	aaa	gtt	tcc	aac	cga	ttt	tct	240
Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	
				50					55					60		

ggg	gtc	cca	gac	agg	ttc	agt	ggc	agt	gga	tca	ggg	aca	gat	ttc	aca	288
Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	
			65				70					75				

ctc	aag	atc	aag	aaa	gtg	gag	gct	gag	gat	ctg	gga	att	tat	tac	tgc	336
Leu	Lys	Ile	Lys	Lys	Val	Glu	Ala	Glu	Asp	Leu	Gly	Ile	Tyr	Tyr	Cys	
		80				85						90				

ttt	caa	ggt	tca	cat	gtt	ccg	ctc	acg	ttc	ggt	gct	ggg	acc	aag	ctg	384
Phe	Gln	Gly	Ser	His	Val	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	
	95					100				105						

gag	ctg	gaa														393
Glu	Leu	Glu														
110																

<210> 14

<211> 131

<212> PRT

<213> Mus musculus

<220>

<221> SIGNAL

<222> (1)...(19)

<400> 14

Met	Lys	Leu	Pro	Val	Arg	Leu	Leu	Val	Leu	Met	Phe	Trp	Ile	Pro	Ala	
				-15					-10					-5		
Ser	Ser	Ser	Asp	Val	Leu	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	
			1			5					10					
Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Asn	Ile	
	15					20				25						
Ile	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	Glu	Trp	Tyr	Leu	Gln	Lys	Pro	
	30				35				40					45		
Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	
				50					55					60		
Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	
			65				70					75				

Leu Lys Ile Lys Lys Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
 80 85 90
 Phe Gln Gly Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
 95 100 105
 Glu Leu Glu
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<210> 15
 <211> 426
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(426)
 <221> sig_peptide
 <222> (1)...(57)

<400> 15
 atg gac agg ctt act tcc tca ttc ctg ctg ctg att gtc cct gca tat 48
 Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
 -15 -10 -5
 gtc ctg tcc cag gct act ctg aaa gag tct ggc cct gga ata ttg cag 96
 Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
 1 5 10
 tcc tcc cag acc ctc agt ctg act tgt tct ttc tct ggg ttt tca ctg 144
 Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
 15 20 25
 agc act tct ggt atg gga gtg agc tgg att cgt cag cct tca gga aag 192
 Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
 30 35 40 45
 ggt ctg gag tgg ctg gca cac att tac tgg gat gat gac aag cgc tat 240
 Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
 50 55 60
 aac cca tcc ctg aag agc cgg ctc aca atc tcc aag gat acc tcc aga 288
 Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
 65 70 75
 aag cag gta ttc ctc aag atc acc agt gtg gac cct gca gat act gcc 336
 Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala
 80 85 90
 aca tac tac tgt gtt cga agg ccc att act ccg gta cta gtc gat gct 384
 Thr Tyr Tyr Cys Val Arg Arg Pro Ile Thr Pro Val Leu Val Asp Ala
 95 100 105
 atg gac tac tgg ggt caa gga acc tca gtc acc gtc tcc tca 426
 Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 110 115 120

<210> 16
 <211> 142
 <212> PRT
 <213> Mus musculus

<220>
 <221> SIGNAL
 <222> (1)...(19)

<400> 16
 Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
 -15 -10 -5
 Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
 1 5 10
 Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
 15 20 25
 Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
 30 35 40 45
 Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
 50 55 60
 Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
 65 70 75
 Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala
 80 85 90
 Thr Tyr Tyr Cys Val Arg Arg Pro Ile Thr Pro Val Leu Val Asp Ala
 95 100 105
 Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 110 115 120

<210> 17
 <211> 136
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 17
 tccgcaagct tgccgcccacc atggacatgc gcgtgcccgc ccagctgctg ggcctgctga 60
 tgctgtgggt gtccggctcc tccggctacg tggatgatgac ccagtccccc ctgtccctgc 120
 ccgtgacccc cggcga 136

<210> 18
 <211> 131
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 18
 ctgggggggac tggccgggct tctgcagcag ccagttcagg taggtcttgc cgtcggagtc 60
 cagcaggggac tgggaggact tgcaggagat ggaggcgggc tcgccggggg tcacgggcag 120
 ggacaggggg g 131

<210> 19
 <211> 146
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 19
 acctgaactg gctgctgcag aagcccggcc agtcccccca gcgcctgata tacctgggtgt 60
 ccaagctgga ctccggcgtg cccgaccgct tctccggctc cggtccggc accgacttca 120
 ccctgaagat ctcccgctg gaggcc 146

<210> 20
 <211> 142
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 20
 aattctagga tccactcacg ctgatctcc accttgggtgc cctggccgaa ggtgcggggg 60
 aagtgggtgc cctgccagca gtagtacacg cccacgtcct cggcctccac gcgggagatc 120
 ttcagggtga agtcggtgcc gg 142

<210> 21
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 21
 ctggggggac tggccg 16

<210> 22
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 22
 acctgaactg gctgctgcag aa 22

<210> 23
 <211> 138
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 23
 acagaaagct tgccgccacc atggagtttg ggctgagctg gctttttctt gtggctatatt 60
 taaaagggtgt ccagtgtgag gtgcagctgc tggagtcgg cggcggcctg gtgcagcccg 120
 gcggctccct gcgcctgt 138

<210> 24
 <211> 135
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 24
 gccgccggag eggatggagg ccacccactc caggcccttg ccggggggcct ggcgcaccca 60
 ggacatgccg tagttggaga aggtgaagcc ggaggcggcg caggacaggc gcaggggagcc 120
 gccgggctgc accag 135

<210> 25
 <211> 142
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 25
 ctggagtggg tggcctccat ccgctccggc ggccggccgca cctactactc cgacaacgtg 60
 aagggccgct tcaccatctc ccgcgcacaac gccagaact ccctgtacct gcagatgaac 120
 tccctgcgcg ccgaggacac cg 142

<210> 26
 <211> 144
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 26
 ctgcaaggat ccaactcacg gaggacacgg tcaccagggt gccctggccc cagtagtcgg 60
 aggagccgga gtagtggtcg tagcgcacgc agtagtacag ggcggtgtcc tcggcgcgca 120
 gggagttcat ctgcaggtac aggg 144

<210> 27
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 27
 gccgccggag cggatg 16

<210> 28
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 28
 ctggagtggg tggcctccat 20

<210> 29
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 29
 tccgcaagct tgccgccac 19

<210> 30
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 30
 aattctagga tccactcacg cttgatctc 29

<210> 31
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 31
 acagaaagct tgccgccacc atg 23

<210> 32
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 32
 ctgcaaggat ccaactcaccg ga 22

<210> 33
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> native ABeta peptide

<400> 33
 Asp Ala Glu Phe Arg His Asp Ser Gly Tyr
 1 5 10

<210> 34
 <211> 402
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> h3D6 version 1 VL

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20     25     30
Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35     40     45
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50     55     60
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65     70     75     80
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85     90     95
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100    105    110
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115    120    125
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130    135    140
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145    150    155    160
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165    170    175
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180    185    190
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195    200    205
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
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245    250    255
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260    265    270
Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275    280    285
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290    295    300
Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305    310    315    320
Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
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Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg	Glu	Trp	Glu	Glu	Ala	405	410	415	
Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	Lys	Lys	Ala	Val	Ile	420	425	430	
Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	Gln	Glu	Ala	Ala	Asn	435	440	445	
Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala	Arg	Val	Glu	Ala	Met	450	455	460	
Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	Tyr	Ile	Thr	Ala	Leu	465	470	475	480
Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	Asn	Met	Leu	Lys	Lys	485	490	495	
Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	Thr	Leu	Lys	His	Phe	500	505	510	
Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	Ala	Gln	Ile	Arg	Ser	515	520	525	
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Glu	Val	Asp	Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn	Tyr	Ser	Asp	Asp	Val	565	570	575	
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Val	Met	Leu	Lys	Lys	Lys	Gln	Tyr	Thr	Ser	Ile	His	His	Gly	Val	Val	725	730	735	
Glu	Val	Asp	Ala	Ala	Val	Thr	Pro	Glu	Glu	Arg	His	Leu	Ser	Lys	Met	740	745	750	
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